



(i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.
(ii) TITLE OF INVENTION: Novel Polypeptide Having Water Channel Activity and DNA sequence
(iii) NUMBER OF SEQUENCES: 2
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.
(B) STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku
(C) CITY: Osaka
(D) STATE: Osaka
(E) COUNTRY: JAPAN
(F) ZIP: 533-0021
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage
(B) COMPUTER: IBM PS/2 or compatibles
(C) OPERATING SYSTEM: WINDOWS 95/97
(D) SOFTWARE: Microsoft Word 97
(vi) CURRENT APPLICATION DATE:
(A) APPLICATION NUMBER: 09/381,810
(B) FILING DATE: 19-OCT-1999
(C) CLASSIFICATION: 435
(vii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: PCT/JP98/01371
(B) FILING DATE: 27-MAR-1998
(C) APPLICATION NUMBER: JP 09-094845
(D) FILING DATE: 28-MAR-1997
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Burton A. Amernick
(B) REGISTRATION NUMBER: 24852
(C) REFERENCE/DOCKET NUMBER: 1581/00156
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202)331-7111
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH F342 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY F linear
(ii) MOLECULE TYPE F peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met
5 10 15
Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys
20 25 30
Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met
35 40 45
Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr
50 55 60
Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Val Thr Met
65 70 75 80
Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala

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85	90	95	
Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe			
100	105	110	
Pro Val Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala			
115	120	125	
Thr Ile Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly			
130	135	140	
Gln Leu Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr			
145	150	155	160
Tyr Leu Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala			
165	170	175	
Trp Leu Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln			
180	185	190	
Glu Asn Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile			
195	200	205	
Leu Val Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala			
210	215	220	
Ile Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala			
225	230	235	240
Gly Trp Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val			
245	250	255	
Pro Val Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr			
260	265	270	
Leu Val Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu			
275	280	285	
Asp Ser Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met			
290	295	300	
Gly Ser His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser			
305	310	315	320
Pro Ala Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser			
325	330	335	
Met Ala Leu Glu His Phe			
340			

(2) INFORMATION FOR SEQ ID No F2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH F1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY F linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) TISSUE TYPE: fat tissue

(ix) @FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION F173..1198
- (C) IDENTIFICATION METHOD: by experiment

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGCTCTGGAC	TGGGGACACA	GGGATAGCTG	AGCCCCAGCT	GGGGGTGGAA	GCTGAGCCAG	60
GGACAGTCAC	GGAGGAACAA	GATCAAGATG	CGCTGTAATC	GAGAAGCCCC	CAAGGCGGAG	120
GCTGAGAACAT	AGAGACATTT	CAGCAGACAT	CTACAAATCT	GAAAGACAAA	AC ATG GTT	178
				Met	Val	

1

CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC	226
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Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser	5	10	15	
TGG TCC GTG ATA GCA AAG ATC CAG GAA ATA CTG CAG AGG AAG ATG GTG				274
Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys Met Val	20	25	30	
CGA GAG TTC CTG GCC GAG TTC ATG AGC ACA TAT GTC ATG ATG GTA TTC				322
Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met Val Phe	35	40	45	50
GGC CTT GGT TCC GTG GCC CAT ATG GTT CTA AAT AAA AAA TAT GGG AGC				370
Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr Gly Ser	55	60	65	
TAC CTT GGT GTC AAC TTG GGT TTT GGC TTC GGA GTC ACC ATG GGA GTG				418
Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met Gly Val	70	75	80	
CAC GTG GCA GGC CGC ATC TCT GGA GCC CAC ATG AAC GCA GCT GTG ACC				466
His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala Val Thr	85	90	95	
TTT GCT AAC TGT GCG CTG GGC CGC GTG CCC TGG AGG AAG TTT CCG GTC				514
Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe Pro Val	100	105	110	
TAT GTG CTG GGG CAG TTC CTG GGC TCC TTC CTG GCG GCT GCC ACC ATC				562
Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala Thr Ile	115	120	125	130
TAC AGT CTC TTC TAC ACG GCC ATT CTC CAC TTT TCG GGT GGA CAG CTG				610
Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly Gln Leu	135	140	145	
ATG GTG ACC GGT CCC GTC GCT ACA GCT GGC ATT TTT GCC ACC TAC CTT				658
Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu	150	155	160	
CCT GAT CAC ATG ACA TTG TGG CGG GGC TTC CTG AAT GAG GCG TGG CTG				706
Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu	165	170	175	
ACC GGG ATG CTC CAG CTG TGT CTC TTC GCC ATC ACG GAC CAG GAG AAC				754
Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln Glu Asn	180	185	190	
AAC CCA GCA CTG CCA GGA ACA GAG GCG CTG GTG ATA GGC ATC CTC GTG				802
Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val	195	200	205	210
GTC ATC ATC GGG GTG TCC CTT GGC ATG AAC ACA GGA TAT GCC ATC AAC				850
Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile Asn	215	220	225	
CCG TCC CGG GAC CTG CCC CGC ATC TTC ACC TTC ATT GCT GGT TGG				898
Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala Gly Trp	230	235	240	
GGC AAA CAG GTC TTC AGC AAT GGG GAG AAC TGG TGG TGG GTG CCA GTG				946
Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val Pro Val	245	250	255	
GTG GCA CCA CTT CTG GGT GCC TAT CTA GGT GGC ATC ATC TAC CTG GTC				994
Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Ile Ile Tyr Leu Val	260	265	270	
TTC ATT GGC TCC ACC ATC CCA CGG GAG CCC CTG AAA TTG GAG GAT TCT				1042
Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu Asp Ser	275	280	285	290
GTG GCG TAT GAA GAC CAC GGG ATA ACC GTA TTG CCC AAG ATG GGA TCT				1090
Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met Gly Ser	295	300	305	
CAT GAA CCC ACG ATC TCT CCC CTC ACC CCC GTC TCT GTG AGC CCT GCC				1138

His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser Pro Ala
310 315 320
AAC AGA TCT TCA GTC CAC CCT GCC CCA CCC TTA CAT GAA TCC ATG GCC 1186
Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser Met Ala
325 330 335
CTA GAG CAC TTC TAAGCAGAGA TTATTTGTGA TCCCCATCCAT TCCCCAATAA 1238
Leu Glu His Phe
340
AGCAAGGCTT GTCCGACAAA 1258